

EXHIBIT 5

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Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.15 [Oct-15-2006]

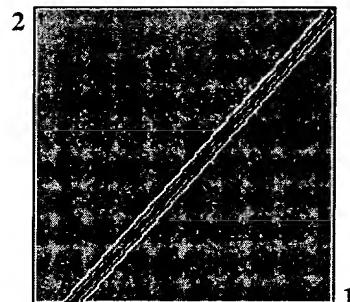
Matrix BLOSUM62 gap open: 11 gap extension: 1x_dropoff: 50 expect: 10.000 wordsize: 3 Filter View option Standard Masking character option X for protein, n for nucleotide Masking color option Black Show CDS translation Align

Sequence 1: gi|1469860|dbj|BAA09787.1|leptin [Homo sapiens] >gi|4557715|ref|NP_000221.1| leptin precursor [Homo sapiens] >gi|730218|sp|P41159|LEP_HUMAN Leptin precursor (Obesity factor) (Obese protein) >gi|623332|gb|AAA60470.1| ob >gi|1226244|gb|AAC50400.1| obese protein >gi|1407583|dbj|BAA09839.1| ob protein [Homo sapiens] >gi|38174530|gb|AAH60830.1| Leptin (obesity homolog, mouse) [Homo sapiens] >gi|46854318|gb|AAH69527.1| Leptin (obesity homolog, mouse) [Homo sapiens] >gi|46854679|gb|AAH69452.1| Leptin (obesity homolog, mouse) [Homo sapiens]...

Length = 167 (1 .. 167)

Sequence 2: gi|110666863|gb|ABG81864.1|obese protein [Anguilla japonica]

Length = 146 (1 .. 146)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 241 bits (615), Expect = 1e-62
 Identities = 123/145 (84%), Positives = 136/145 (93%), Gaps = 0/145 (0%)

Query 23	PIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTLGLDFIPGLHPILTLSKMDQTLAVY	82
Sbjct 2	PIQKVQDDTKTLIKTIVTRINDISHTQSVS+KQ+VTGLDFIPGLHPIL+LSKMDQTLAVY	61
Query 83	QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST	142
Sbjct 62	QQVLTSLPSQNVLQIANDLENLRDLLHLLAFSKCSLSPQTSGLQKPESLDGVLEASLYST	121
Query 143	EVVALSRLQGSLQDMLWQLDLSPGC 167	
Sbjct 122	EVVALSRLQGSLQDILQQLDVSPEC 146	

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

Lambda K H
0.321 0.135 0.415

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 262
Number of extensions: 97
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 167
Length of database: 1,565,033,500
Length adjustment: 124
Effective length of query: 43
Effective length of database: 1,565,033,376
Effective search space: 67296435168
Effective search space used: 67296435168
Neighboring words threshold: 9
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.9 bits)
S2: 73 (32.7 bits)